



SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING
BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10/547,532

<141> 2005-08-31

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(288)

<223> Human MIP-3.alpha. cDNA

<220>

<221> sig_peptide

<222> (1)..(78)

<223> Human MIP-3.alpha. cDNA

<220>

<221> mat_peptide

<222> (79)..()

<223> Human MIP-3.alpha. cDNA

<400> 1

atg tgc tgt acc aag agt ttg ctc ctg gct gct ttg atg tca gtg ctg	48
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
-25 -20 -15	
cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc	96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10 -5 -1 1 5	
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc	144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10 15 20	
ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc	192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
25 30 35	
ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act	240
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
40 45 50	
tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg	288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
55 60 65 70	

<210> 2
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -25 -20 -15
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 -1 1
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

<210> 3
 <211> 288
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1)..(288)
 <223> Rat MIP-3.alpha. cDNA

<220>
 <221> sig_peptide
 <222> (1)..(75)
 <223> Rat MIP-3.alpha. cDNA

<220>
 <221> mat_peptide
 <222> (76)..()
 <223> Rat MIP-3.alpha. cDNA

<400> 3
 atg gcc tgc aag cat ctg ccc ttc ctg gct ttg gcg ggg gta ctg ctg 48
 Met Ala Cys Lys His Leu Pro Phe Leu Ala Leu Ala Gly Val Leu Leu
 -25 -20 -15
 gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96
 Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
 -5 -1 1 5
 ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt 144
 Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
 10 15 20
 ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc 192
 Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc 240
 Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
 40 45 50 55
 tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc aag aag atg 288
 Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
 60 65 70

<210> 4
 <211> 96
 <212> PRT
 <213> Rattus norvegicus

<400> 4
Met Ala Cys Lys His Leu Pro Phe Leu Ala Leu Ala Gly Val Leu Leu
-25 -20 -15 -10
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
-5 -1 1 5
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
10 15 20
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
25 30 35
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
40 45 50 55
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
60 65 70

<210> 5
<211> 291
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(291)
<223> Mouse MIP-3.alpha. cDNA

<220>
<221> sig_peptide
<222> (1)..(81)
<223> Mouse MIP-3.alpha. cDNA

<220>
<221> mat_peptide
<222> (82)..()
<223> Mouse MIP-3.alpha. cDNA

<400> 5
atg gcc tgc ggt ggc aag cgt ctg ctc ttc ctt gct ttg gca tgg gta 48
Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val
-25 -20 -15
ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac 96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp
-10 -5 -1 1 5
tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg 144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
10 15 20
ggt ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc 192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
25 30 35
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag 240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
40 45 50
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag 288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
55 60 65
atg 291
Met
70

<210> 6
<211> 97
<212> PRT
<213> Mus musculus

<400> 6

Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val
 -25 -20 -15
 Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp
 -10 -5 1 1 5
 Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
 10 15 20
 Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
 25 30 35
 Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
 40 45 50
 Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
 55 60 65
 Met
 70

<210> 7
 <211> 1122
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1122)
 <223> Human CCR6 cDNA

<400> 7
 atg agc ggg gaa tca atg aat ttc agc gat gtt ttc gac tcc agt gaa 48
 Met Ser Gly Glu Ser Met Asn Phe Ser Asp Val Phe Asp Ser Ser Glu
 1 5 10 15
 gat tat ttt gtg tca gtc aat act tca tat tac tca gtt gat tct gag 96
 Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
 20 25 30
 atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt 144
 Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
 35 40 45
 gta ccg att gcc tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat 192
 Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
 50 55 60
 att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg 240
 Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
 65 70 75 80
 aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt 288
 Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
 85 90 95
 ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt 336
 Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
 100 105 110
 ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac 384
 Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
 115 120 125
 ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac 432
 Phe Asn Cys Gly Met Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
 130 135 140
 atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca 480
 Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
 145 150 155 160
 cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc 528
 Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Trp Gly Leu Ser Val
 165 170 175
 atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa 576
 Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
 180 185 190
 ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc 624
 Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile

	195		200		205														
agg	tgg	aag	ctg	ctg	atg	ttg	ggg	ctt	gag	cta	ctc	ttt	ggg	ttc	ttt				
Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu	Glu	Leu	Leu	Phe	Gly	Phe	Phe				672
	210					215					220								
atc	cct	ttg	atg	ttc	atg	ata	ttt	tgt	tac	acg	ttc	att	gtc	aaa	acc				720
Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys	Tyr	Thr	Phe	Ile	Val	Lys	Thr				
	225					230				235					240				
ttg	gtg	caa	gct	cag	aat	tct	aaa	agg	cac	aaa	gcc	atc	cgt	gta	atc				768
Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg	His	Lys	Ala	Ile	Arg	Val	Ile				
				245					250					255					
ata	gct	gtg	gtg	ctt	gtg	ttt	ctg	gct	tgt	cag	att	cct	cat	aac	atg				816
Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala	Cys	Gln	Ile	Pro	His	Asn	Met				
			260					265					270						
gtc	ctg	ctt	gtg	acg	gct	gca	aat	ttg	ggg	aaa	atg	aac	cga	tcc	tgc				864
Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu	Gly	Lys	Met	Asn	Arg	Ser	Cys				
			275				280					285							
cag	agc	gaa	aag	cta	att	ggc	tat	acg	aaa	act	gtc	aca	gaa	gtc	ctg				912
Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr	Lys	Thr	Val	Thr	Glu	Val	Leu				
	290					295					300								
gct	ttc	ctg	cac	tgc	tgc	ctg	aac	cct	gtg	ctc	tac	gct	ttt	att	ggg				960
Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Ile	Gly				
	305			310						315					320				
cag	aag	ttc	aga	aac	tac	ttt	ctg	aag	atc	ttg	aag	gac	ctg	tgg	tgt				1008
Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	Ile	Leu	Lys	Asp	Leu	Trp	Cys				
			325					330					335						
gtg	aga	agg	aag	tac	aag	tcc	tca	ggc	ttc	tcc	tgt	gcc	ggg	agg	tac				1056
Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly	Phe	Ser	Cys	Ala	Gly	Arg	Tyr				
			340					345					350						
tca	gaa	aac	att	tct	cgg	cag	acc	agt	gag	acc	gca	gat	aac	gac	aat				1104
Ser	Glu	Asn	Ile	Ser	Arg	Gln	Thr	Ser	Glu	Thr	Ala	Asp	Asn	Asp	Asn				
		355				360						365							
gcg	tcg	tcc	ttc	act	atg														1122
Ala	Ser	Ser	Phe	Thr	Met														
	370																		

<210> 8
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ser Gly Glu Ser Met Asn Phe Ser Asp Val Phe Asp Ser Ser Glu
 1 5 10 15
 Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
 20 25 30
 Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
 35 40 45
 Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
 50 55 60
 Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
 65 70 75 80
 Thr Asp Val Tyr Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
 85 90 95
 Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
 100 105 110
 Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
 115 120 125
 Phe Asn Cys Gly Met Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
 130 135 140
 Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
 145 150 155 160
 Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
 165 170 175
 Ile Ile Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
 5

Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr	Gln	Thr	Val	Ser	Glu	Pro	Ile
Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu	Glu	Leu	Leu	Phe	Gly	Phe	Phe
Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys	Tyr	Thr	Phe	Ile	Val	Lys	Thr
Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg	His	Lys	Ala	Ile	Arg	Val	Ile
Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala	Cys	Gln	Ile	Pro	His	Asn	Met
Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu	Gly	Lys	Met	Asn	Arg	Ser	Cys
Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr	Lys	Thr	Val	Thr	Glu	Val	Leu
Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Ile	Gly
Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	Ile	Leu	Lys	Asp	Leu	Trp	Cys
Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly	Phe	Ser	Cys	Ala	Gly	Arg	Tyr
Ser	Glu	Asn	Ile	Ser	Arg	Gln	Thr	Ser	Glu	Thr	Ala	Asp	Asn	Asp	Asn
Ala	Ser	Ser	Phe	Thr	Met										

<210> 9
 <211> 1101
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1101)
 <223> Mouse CCR6 cDNA

atg	aat	tcc	aca	gag	tcc	tac	ttt	gga	acg	gat	gat	tat	gac	aac	aca	48
Met	Asn	Ser	Thr	Glu	Ser	Tyr	Phe	Gly	Thr	Asp	Asp	Tyr	Asp	Asn	Thr	
1			5						10				15			
gag	tat	tat	tct	att	cct	cca	gac	cat	ggg	cca	tgc	tcc	cta	gaa	gag	96
Glu	Tyr	Tyr	Ser	Ile	Pro	Pro	Asp	His	Gly	Pro	Cys	Ser	Leu	Glu	Glu	
			20					25					30			
gtc	aga	aac	ttc	acc	aag	gta	ttt	gtg	cca	att	gcc	tac	tcc	tta	ata	144
Val	Arg	Asn	Phe	Thr	Lys	Val	Phe	Val	Pro	Ile	Ala	Tyr	Ser	Leu	Ile	
			35				40				45					
tgt	gtc	ttt	ggc	ctc	ctg	ggc	aac	att	atg	gtg	gtg	atg	acc	ttt	gcc	192
Cys	Val	Phe	Gly	Leu	Leu	Gly	Asn	Ile	Met	Val	Val	Met	Thr	Phe	Ala	
			50			55					60					
ttc	tac	aag	aaa	gcc	aga	tcc	atg	act	gac	gtc	tac	ctg	ttg	aac	atg	240
Phe	Tyr	Lys	Lys	Ala	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	
					70				75					80		
gcc	atc	aca	gac	ata	ctc	ttt	gtc	ctc	acc	cta	ccg	ttc	tgg	gca	gtt	288
Ala	Ile	Thr	Asp	Ile	Leu	Phe	Val	Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	
				85				90						95		
act	cat	gcc	acc	aac	act	tgg	gtt	ttc	agc	gat	gca	ctg	tgt	aaa	ctg	336
Thr	His	Ala	Thr	Asn	Thr	Trp	Val	Phe	Ser	Asp	Ala	Leu	Cys	Lys	Leu	
			100					105					110			
atg	aaa	ggc	aca	tat	gcg	gtc	aac	ttt	aac	tgt	ggg	atg	ctg	ctc	ctg	384
Met	Lys	Gly	Thr	Tyr	Ala	Val	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	
			115				120					125				
gcc	tgt	atc	agc	atg	gac	cgg	tac	att	gcc	atc	gtc	cag	gca	acc	aaa	432
Ala	Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	
			130			135					140					

tct	ttc	cgg	gta	cgc	tcc	aga	aca	ctg	acg	cac	agt	aag	gtc	atc	tgt	480
Ser	Phe	Arg	Val	Arg	Ser	Arg	Thr	Leu	Thr	His	Ser	Lys	Val	Ile	Cys	
145					150					155					160	
gtg	gca	gtg	tgg	ttc	atc	tcc	atc	atc	atc	tca	agc	cct	aca	ttt	atc	528
Val	Ala	Val	Trp	Phe	Ile	Ser	Ile	Ile	Ile	Ser	Ser	Pro	Thr	Phe	Ile	
				165					170					175		
ttc	aac	aag	aaa	tac	gag	ctg	cag	gat	cgt	gat	gtc	tgt	gag	cca	cgg	576
Phe	Asn	Lys	Lys	Tyr	Glu	Leu	Gln	Asp	Arg	Asp	Val	Cys	Glu	Pro	Arg	
			180					185					190			
tac	agg	tct	gtc	tca	gag	ccc	atc	acg	tgg	aag	ctg	ctg	ggg	atg	gga	624
Tyr	Arg	Ser	Val	Ser	Glu	Pro	Ile	Thr	Trp	Lys	Leu	Leu	Gly	Met	Gly	
			195				200					205				
ctg	gag	ctg	ttc	ttt	ggg	ttc	ttc	acc	cct	ttg	ctg	ttt	atg	gtg	ttc	672
Leu	Glu	Leu	Phe	Phe	Gly	Phe	Phe	Thr	Pro	Leu	Leu	Phe	Met	Val	Phe	
			210			215					220					
tgc	tat	ctg	ttc	att	atc	aag	acc	ttg	gtg	cag	gcc	cag	aac	tcc	aag	720
Cys	Tyr	Leu	Phe	Ile	Ile	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	
				230						235					240	
agg	cac	aga	gcc	atc	cga	gtc	gtg	atc	gct	gtg	gtt	ctc	gtg	ttc	ctg	768
Arg	His	Arg	Ala	Ile	Arg	Val	Val	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	
				245					250					255		
gct	tgt	cag	atc	cct	cac	aac	atg	gtc	ctc	ctc	gtg	act	gcg	gtc	aac	816
Ala	Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Val	Asn	
			260					265					270			
acg	ggc	aaa	gtg	ggc	cgg	agc	tgc	agc	acc	gag	aaa	gtc	ctc	gcc	tac	864
Thr	Gly	Lys	Val	Gly	Arg	Ser	Cys	Ser	Thr	Glu	Lys	Val	Leu	Ala	Tyr	
			275				280					285				
acc	agg	aac	gtg	gcc	gag	gtc	ctg	gct	ttc	ctg	cat	tgc	tgc	ctc	aac	912
Thr	Arg	Asn	Val	Ala	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	
			290			295					300					
ccc	gtg	ttg	tat	gcg	ttt	att	gga	cag	aaa	ttc	aga	aac	tac	ttc	atg	960
Pro	Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Met	
				310					315						320	
aag	atc	atg	aag	gat	gtg	tgg	tgt	atg	aga	agg	aag	aat	aag	atg	cct	1008
Lys	Ile	Met	Lys	Asp	Val	Trp	Cys	Met	Arg	Arg	Lys	Asn	Lys	Met	Pro	
				325					330					335		
ggc	ttc	ctc	tgt	gcc	cgg	gtt	tac	tcg	gaa	agc	tac	atc	tcc	agg	cag	1056
Gly	Phe	Leu	Cys	Ala	Arg	Val	Tyr	Ser	Glu	Ser	Tyr	Ile	Ser	Arg	Gln	
			340					345					350			
acc	agt	gag	acc	gtc	gaa	aat	gat	aat	gca	tcg	tcc	ttt	acc	atg		1101
Thr	Ser	Glu	Thr	Val	Glu	Asn	Asp	Asn	Ala	Ser	Ser	Phe	Thr	Met		
			355				360					365				

<210> 10
 <211> 367
 <212> PRT
 <213> Mus musculus

<400> 10
 Met Asn Ser Thr Glu Ser Tyr Phe Gly Thr Asp Asp Tyr Asp Asn Thr
 1 5 10 15
 Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
 20 25 30
 Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
 35 40 45
 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
 50 55 60
 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75
 Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
 85 90 95
 Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
 100 105 110
 Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu

Ala	Cys	115	Ile	Ser	Met	Asp	Arg	120	Tyr	Ile	Ala	Ile	Val	125	Gln	Ala	Thr	Lys
Ser	Phe	130	Arg	Val	Arg	Ser	Arg	135	Thr	Leu	Thr	His	Ser	140	Lys	Val	Ile	Cys
Val	Ala	145	Val	Trp	Phe	Ile	Ser	150	Ile	Ile	Ile	Ser	Ser	155	Pro	Thr	Phe	Ile
Phe	Asn	165	Lys	Tyr	Glu	Leu	Gln	170	Asp	Arg	Asp	Val	Cys	175	Glu	Pro	Arg	
Tyr	Arg	180	Ser	Val	Ser	Glu	Pro	185	Thr	Trp	Lys	Leu	Leu	190	Gly	Met	Gly	
Leu	Glu	195	Leu	Phe	Phe	Gly	Phe	200	Thr	Pro	Leu	Leu	Phe	205	Met	Val	Phe	
Cys	Tyr	210	Leu	Phe	Ile	Ile	Lys	215	Thr	Leu	Val	Gln	Ala	220	Gln	Asn	Ser	Lys
Arg	His	225	Arg	Ala	Ile	Arg	Val	230	Val	Ile	Ala	Val	Val	235	Leu	Val	Phe	Leu
Ala	Cys	245	Gln	Ile	Pro	His	Asn	250	Met	Val	Leu	Leu	Val	255	Thr	Ala	Val	Asn
Thr	Gly	260	Lys	Val	Gly	Arg	Ser	265	Cys	Ser	Thr	Glu	Lys	270	Val	Leu	Ala	Tyr
Thr	Arg	275	Asn	Val	Ala	Glu	Val	280	Leu	Ala	Phe	Leu	His	285	Cys	Cys	Leu	Asn
Pro	Val	290	Leu	Tyr	Ala	Phe	Ile	295	Gly	Gln	Lys	Phe	Arg	300	Asn	Tyr	Phe	Met
Lys	Ile	305	Met	Lys	Asp	Val	Trp	310	Cys	Met	Arg	Arg	Lys	315	Asn	Lys	Met	Pro
Gly	Phe	325	Leu	Cys	Ala	Arg	Val	330	Tyr	Ser	Glu	Ser	Tyr	335	Ile	Ser	Arg	Gln
Thr	Ser	340	Glu	Thr	Val	Glu	Asn	345	Asp	Asn	Ala	Ser	Ser	350	Phe	Thr	Met	
		355						360						365				

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> misc_feature
 <223> Oligonucleotide designed to act as primer for amplifying fragment of rat MIP-3.alpha. gene transcript.

<400> 11
 agaatggcct gcaagcatct 20

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> misc_feature
 <223> Oligonucleotide designed to act as primer for amplifying fragment of rat MIP-3.alpha. gene transcript.

<400> 12
 tgcagaggta agccagcagt a 21

<210> 13
 <211> 1502
 <212> DNA
 <213> Rattus norvegicus (kidney)

<220>

<221> CDS
 <222> (343)..(1443)
 <223> Rat kidney-derived CCR6 cDNA

<400> 13

tgtattgaag	acagaacact	tgttggaaga	cacccacccc	cgggagggcg	aagaacaagc	60
cacacactgc	tttgaagagt	ccagccccc	gcagaactgc	aagggcagac	actgttctgg	120
ccacctgcag	tttgaagtca	tcactttcaa	tccccctgtg	actagggcca	gggtcttcac	180
acctgcgaga	ggaagcaaag	atctaagcaa	tctgaatttt	aagagagaaa	ctgcagctgt	240
cggtttggtg	gccggaacat	tattggactg	gagcctggac	aagcactaag	gcgggggtac	300
ctggccagcc	cacttcggag	ctcagcgttt	ccttgggaaa	cg atg aat ttc acc		354

Met Asn Phe Thr
1

gag gcc aac tac gga atg gaa gat tat act ggc tca gat tac tct atg	402
Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met	
5 10 15 20	
ttt cca gag acc gag cca tgc tct ctg caa gag gtc aga gac ttc acc	450
Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val Arg Asp Phe Thr	
25 30 35	
aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc	498
Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu	
40 45 50	
ctt ggc aat att atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc	546
Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala	
55 60 65	
agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca gac ata	594
Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile	
70 75 80	
ctc ttt gtc ctc acc cta cca ttc tgg gca gtt act cat gcc act gac	642
Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp	
85 90 95 100	
act tgg atc ttt ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat	690
Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr	
105 110 115	
gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg	738
Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met	
120 125 130	
gac cgg tac att gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc	786
Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg	
135 140 145	
tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc	834
Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe	
150 155 160	
gtt tcc atc atc atc tca agc ccc aca ttc ttc ttc aac aag caa tac	882
Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr	
165 170 175 180	
aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg	930
Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser	
185 190 195	
gag ccc atc acg tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt	978
Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe	
200 205 210	
ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc	1026
Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile	
215 220 225	
atc aag acc ttg gtg cag gcc cag aat tcc aag agg cac aga gcc atc	1074
Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile	
230 235 240	
cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct	1122
Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro	
245 250 255 260	
cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc	1170
His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly	
265 270 275	

cgc agc tgc agc gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct	1218
Arg Ser Cys Ser 280 Ala Glu Lys Ala Leu 285 Ala Tyr Ala Arg Asn Val Ala	
gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc	1266
Glu Val Leu Ala Phe Leu His Cys 300 Cys Leu Asn Pro Val Leu Tyr Ala	
ttc att gga cag aaa ttc aga agc tac ttc atg aag atc atg aag gat	1314
Phe Ile Gly Gln Lys Phe Arg 315 Ser Tyr Phe Met Lys 320 Ile Met Lys Asp	
gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc ttc tgt gcc	1362
Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro 335 Thr Phe Phe Cys Ala 340	
cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta	1410
Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg 350 Gln Thr Ser Glu Thr Val 355	
gaa aat gac aac gca tcg tcc ttt acc atg taa cacgagagca caaagcagca	1463
Glu Asn Asp Asn Ala Ser Ser Phe Thr Met 365	
tgccccgaaa gcctttgtga aacttgctat tacatgtga	1502

<210> 14
 <211> 366
 <212> PRT
 <213> Rattus norvegicus

<400> 14	
Met Asn Phe Thr Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser	
1 5 10 15	
Asp Tyr Ser Met Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val	
20 25 30	
Arg Asp Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys	
35 40 45	
Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe	
50 55 60	
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala	
65 70 75 80	
Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr	
85 90 95	
His Ala Thr Asp Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met	
100 105 110	
Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Ala	
115 120 125	
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser	
130 135 140	
Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu	
145 150 155 160	
Thr Val Trp Phe Val Ser Ile Ile Ile Ser 170 Pro Thr Phe Phe Phe	
165 175	
Asn Lys Gln Tyr Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr	
180 185 190	
Lys Leu Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu	
195 200 205	
Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys	
210 215 220	
Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg	
225 230 235 240	
His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala	
245 250 255	
Cys Gln Ile Pro His Asn Met Val Leu Val Thr Ala Ala Asn Thr	
260 265 270	
Gly Lys Met Gly Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala	
275 280 285	
Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys 300 Cys Leu Asn Pro	
290 295	

cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc atc aag acc ttg	845
Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile Ile Lys Thr Leu	
220 230	
gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg att	893
Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile	
235 240 245	
gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct cac aac atg gtc	941
Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met Val	
250 255 260	
ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc agc tgc agc	989
Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys Ser	
265 270 275 280	
gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct	1037
Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala	
285 290 295	
ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc ttc att gga cag	1085
Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly Gln	
300 305 310	
aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt atg	1133
Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met	
315 320 325	
agg agg aag agc aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca	1181
Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala Arg Val Tyr Ser	
330 335 340	
gaa agc tac atc tcc agg cag acc agt gag act gta gaa aat gac aac	1229
Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp Asn	
345 350 355 360	
gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa	1280
Ala Ser Ser Phe Thr Met	
365	
gcctttgtga aacttgctat tacatgtga	1309

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide designed to act as primer for amplifying CCR6
 cDNA derived from rat kidney.

<400> 16	
tgtattgaag acagaacact tgtgg	25

<210> 17
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide designed to act as primer for amplifying CCR6
 cDNA derived from rat kidney or rat liver.

<400> 17	
tcacatgtaa tagcaagttt cacaaagg	28

<210> 18
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide designed to act as primer for amplifying CCR6
 cDNA derived from rat liver.

<400> 18
 gcatctcact acccgctctt c 21
 <210> 19
 <211> 21
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide designed to act as primer for amplifying fragment
 of rat CCR6 gene transcript.
 <400> 19
 ggacgatgcg ttgtcatttt c 21
 <210> 20
 <211> 22
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide designed to act as primer for amplifying fragment
 of rat CCR6 gene transcript.
 <400> 20
 ccgcagctgc agcgccgaga aa 22
 <210> 21
 <211> 20
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide designed to act as primer for amplifying fragment
 of rat CCR6 gene transcript.
 <400> 21
 gtgcccgggt ttactcagaa 20